AMENDMENT

Please amend the application without prejudice, without admission, without surrender of subject matter, and without any intention of creating any estoppel as to equivalents, as follows.

In the Specification

Please replace the paragraph beginning on page 6, line 5, with the following rewritten paragraph:

--Hybridization probes which can be used are, for example, nucleic acid molecules which have exactly ore essentially the nucleotide sequence stated under SEQ ID NOs:1, 2 or 6 or parts of these sequences. The fragments used as hybridization probes may also be synthetic fragments which have been prepared with the aid of the customary synthetic techniques whose sequence essentially agrees with that of a nucleic acid molecule according to the invention.--

D1

Please replace the paragraph beginning on page 30, line 6, with the following rewritten paragraph:

--The DNA fragment employed as a probe for screening the wheat cDNA library was amplified with the following primers:

D2

sulp-1: 5'-AAAGGCCCAATATTATCCTTTAGG-3' (SEQ ID NO:4)

sulp-2: 5'-GCCATTTCAACCGTTCTGAAGTCGGGAAGTC-3' (SEQ ID NO:5)--

Please replace the paragraphs beginning on page 31, line 28, with the following rewritten paragraphs:

--The insertion of clone TaSU-19 is 2997 bp in length and constitutes a partial cDNA. The nucleotide sequence is shown under SEQ ID NO:2. A comparison with already published sequences revealed that the sequence shown under SEQ ID NO:2 encompasses a coding region which has homologies to isoamylases from other organisms.

D3

Sequence analysis also reveals that two introns are located in the cDNA sequence in position 297-396 (intron 1) and 1618-2144 (intron 2). If these introns are removed, a protein sequence may be derived which exhibits homologies to the protein sequences of isoamylases of other organisms. The amino acid sequence which corresponds to the coding regions of SEQ ID NO:2 is shown under SEQ ID NO:3.--

Please replace the paragraph beginning on page 32, line 32, with the following rewritten paragraph:

--The wheat-specific digoxygenin-labeled sugary probe employed for screening the cDNA library was prepared by means of PCR amplification. The primers employed in this reaction were:

D4 SUSO1: 5'-GCT TTA CGG GTA CAG GTT CG-3' (SEQ ID NO:8), and
SUSO2: 5'-AAT TCC CCG TTT GTG AGC-3' (SEQ ID NO:9)--

Please replace the paragraphs beginning on page 33, line 32, with the following rewritten paragraphs:

--The nucleotide sequence of the cDNA insert in plasmid pTaSU8A was determined by means of the dideoxynucleotide method (SEQ ID NO:6).

The insertion of clone pTaSU8A is 2437 bp in length and constitutes a partial cDNA. A comparison with already published sequences reveals that the sequence shown under SEQ ID NO:6 comprises a coding region which has homologies to isoamylases from other organisms. D5 Equally, the protein sequence derived from the coding region of clone pTaSU8A and shown in SEQ ID NO:7 exhibits homologies to the protein sequences of isoamylases of other organisms. Upon comparison of the sequences of clones pTaSU19 (SEQ ID NO:1) and pTaSU8A (SEQ ID NO:6), a similarity of 96.8% results. Most of the differences regarding the sequences are in the 3'-untranslated region of the cDNAs. The remaining differences regarding the sequences in the coding region lead to different amine acids at a total of 12 positions of the derived protein sequences SEQ ID NOs:3 and 7. The cDNAs contained in pTaSU19 and pTaSU8A are not identical and encode isoforms of the wheat isoamylase.--

Please replace the paragraphs beginning on page 34, line 28, with the following rewritten paragraphs:

--To clone pTa-alpha-SU8A, an approx. 2.2 kb portion of the TaSU8A cDNA, viz. positions 140-2304 of SEQ ID NO:6 was amplified by means of PCR.

D6 The primers employed in this reaction were:
SUEX3: 5'-GCG GTA CCT CTA GAA GGA GAT ATA CAT ATG GCG GAG GAC AGG TAC GCG CTC-3' SEQ ID NO:10, and
SUEX4: 5'-GCT CGA GTC GAC TCA AAC ATC AGG GCG CAA TAC-3' SEQ ID NO:11.--

Please replace the previously filed sequence listing with the enclosed papers entitled --Sequence Listing--.